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## RAW SEQUENCE LISTING

DATE: 07/26/2001

PATENT APPLICATION: US/09/903,770

TIME: 15:19:35

Input Set : A:\203979US.txt

Output Set: N:\CRF3\07262001\I903770.raw

ENTERED

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3 <110> APPLICANT: MOLENAAR, DOUWE
4     VAN DER REST, MICHEL E
5     DRYSCH, ANDRE
7 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCE WHICH CODE FOR THE mdhA GENE
9 <130> FILE REFERENCE: 203976US0X
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/903,770
C--> 11 <141> CURRENT FILING DATE: 2001-07-13
11 <150> PRIOR APPLICATION NUMBER: DE 10032350.2
12 <151> PRIOR FILING DATE: 2000-07-04
14 <160> NUMBER OF SEQ ID NOS: 5
16 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 18
20 <212> TYPE: PRT
21 <213> ORGANISM: Corynebacterium glutamicum
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26 1             5             10             15
29 Gly Gln
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34 <211> LENGTH: 2663
35 <212> TYPE: DNA
36 <213> ORGANISM: Corynebacterium glutamicum
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (536)..(1519)
41 <223> OTHER INFORMATION:
44 <400> SEQUENCE: 2
45 aaggcctttc ttatcgccaa agtgatagtg gatcatgcgc ttggacatgc cagatgcctt      60
47 cgcgattttc tccaatttgg ttctgctaaa accatcctct gcaaaaaatg tcagagcggt      120
49 ggctactacc tcttcagggg ttgcggtgtg tcctgaatca gattcaatga attcgctacc      180
51 ggcctggtct atgttttcgg catctcgacg tgatgtcgcc ataatcgatc aattcctttc      240
53 gggtaacgag aaaacgtgaa ttagaaacgg ggtaaggta aatatcaaag ataacaccat      300
55 cggcaaatcc cagctgacaa ctataaatgg tgcccgatat caggaaaaat tgcttgacac      360
57 cgcgcgccga ttcccccata tgccctaaca tcttgccagg gaggggtaca tattggggca      420
59 attcgggggg aatttttgag tatcgtaag atcacccaaa actggtggct gttctctttt      480
61 aagcgggata gcatgggttc ttagaggacc ccctacaagg attgaggatt gttta atg      538
62                                     Met
63                                     1
65 aat tcc ccg cag aac gtc tcc acc aag aag gtc acc gtc acc ggc gca      586
66 Asn Ser Pro Gln Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly Ala
67             5             10             15
69 gct ggt caa atc tct tat tca ctg ttg tgg cgc atc gcc aac ggt gaa      634
70 Ala Gly Gln Ile Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly Glu
71             20             25             30
73 gta ttc ggc acc gac acc cct gta gaa ctg aaa ctt ctg gag atc cct      682
74 Val Phe Gly Thr Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile Pro

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75	35	40	45	
77	cag gct ctt ggc ggg gca gag ggt gtg gct atg gaa ctt ctg gat tct	730		
78	Gln Ala Leu Gly Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp Ser			
79	50 55 60 65			
81	gcc ttc ccc ctc ctg cga aac atc acc atc acc gcg gat gcc aat gag	778		
82	Ala Phe Pro Leu Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn Glu			
83	70 75 80			
85	gca ttc gac ggc gct aat gcg gcg ttt ttg gtc ggt gcg aag cct cgc	826		
86	Ala Phe Asp Gly Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg			
87	85 90 95			
89	gga aaa ggc gaa gag cgc gca gat ttg ctg gct aac aac ggc aag att	874		
90	Gly Lys Gly Glu Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys Ile			
91	100 105 110			
93	ttc gga cct caa ggt aaa gct atc aat gac aac gcc gca gat gac att	922		
94	Phe Gly Pro Gln Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp Ile			
95	115 120 125			
97	cgt gtc cta gtt gtt gga aac cca gcg aac acc aac gcg ttg att gct	970		
98	Arg Val Leu Val Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala			
99	130 135 140 145			
101	tca gct gcg gcc cca gat gtt cca gca tcc cgc ttc aac gca atg atg	1018		
102	Ser Ala Ala Ala Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met Met			
103	150 155 160			
105	cgc ctt gat cac aac cgt gcg atc tcc cag ctg gcc acc aag ctt ggc	1066		
106	Arg Leu Asp His Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu Gly			
107	165 170 175			
109	cgt gga tct gcg gaa ttt aac aac att gtg gtc tgg gga aat cac tcc	1114		
110	Arg Gly Ser Ala Glu Phe Asn Asn Ile Val Val Trp Gly Asn His Ser			
111	180 185 190			
113	gca acc cag ttc cca gac atc acc tac gca acc gtt ggt gga gaa aag	1162		
114	Ala Thr Gln Phe Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu Lys			
115	195 200 205			
117	gtc act gac ctg gtt gat cac gat tgg tat gtg gag gag ttc att cct	1210		
118	Val Thr Asp Leu Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile Pro			
119	210 215 220 225			
121	cgc gtg gct aac cgt ggc gct gaa atc att gag gtc cgt gga aag tct	1258		
122	Arg Val Ala Asn Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser			
123	230 235 240			
125	tct gca gct tct gca gca tcc tct gcg att gat cac atg cgc gat tgg	1306		
126	Ser Ala Ala Ser Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp Trp			
127	245 250 255			
129	gta cag ggc acc gag gcg tgg tcc tct gcg gca att cct tcc acc ggt	1354		
130	Val Gln Gly Thr Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr Gly			
131	260 265 270			
133	gca tac ggc att cct gag ggc att ttt gtc ggt ctg cca acc gta tcc	1402		
134	Ala Tyr Gly Ile Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val Ser			
135	275 280 285			
137	cgc aac ggt gag tgg gaa atc gtt gaa ggc ctg gag att tcc gat ttc	1450		
138	Arg Asn Gly Glu Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp Phe			
139	290 295 300 305			

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141 cag cgc gcc cgc atc gac gcg aat gct cag gaa ttg cag gcc gag cgc      1498
142 Gln Arg Ala Arg Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu Arg
143              310              315              320
145 gag gca gtg cgc gac ttg ctc taatctttaa cgcattgactt cgettttcga      1549
146 Glu Ala Val Arg Asp Leu Leu
147              325
149 cgccccaacc ctccaacgcg tcaccgtttt caccggctcg gcgctcggca gttcctcgct      1609
151 gtacacgcaa gcggctcaaa ccttggcgaa aaccgcggta gaccgcggca tcgacttggt      1669
153 ttacggtggc ggaaaagtgg ggctcatggg tatcgtcgcg gatgcgttcc tggaatcagg      1729
155 tggcgaagcc tttggcgta tcacggaatc acttatgaag ggtgagcttg ggcatgaaaa      1789
157 gtcaccgaa cttgaaatcg ttctgatata gcacatccgc aagcgtcgca tggcagaact      1849
159 tggcgaatgg tttatcgcca tgcccggttg cgccggcacc ttggaagaac ttttcgaggt      1909
161 ctggacctgg caacagctgg gcattcatca aaagcccgtc gcactttatg atgtcgatgg      1969
163 tttttggcag cccctgctgg aaatgcttga gcagatgacc cagcgtggat ttatcaagcg      2029
165 agacttcttt gagtgcctca tcgtggaatc cgaccgcgat gccctgctaa aggcaatgca      2089
167 gacctggact ccaccagcac caaaatggta actaaattgt gtgctcgacg gtaacgcgcg      2149
169 cgagtatctt gatggaatg gaagccacgc cgttgctcatt gactgtgatg gtttcttcta      2209
171 cttctggggc atcgaaacgt gaaatctcgg tagcatccac atcggtgatg gagctatcaa      2269
173 aaggaatctt gatttcaact agcagggaaa tatctcggg gctgccatcc tcggacacgg      2329
175 tggagtattc cacgaacctg aaccaaccaa tgttgtgcac cgcctttagt catcgtttcg      2389
177 ccacggtcgc agaatcgggtg tccggggcga tcagcgggtc aaagctcacg gcacgaccag      2449
179 aatcgtgctc acggaacaca ccgatgcctc gcgcaacgcg gtcccttagg tggaaccag      2509
181 aggaagggtc agccgcgatg gccagacca ccgcagtgga acctgagggg aatggggagc      2569
183 ggtggacacg gcggccgaaa cgctcgcgga gcaacctgga aacgagtggg agcgaggatc      2629
185 cactagttct agagcggcgc ccaccgcggt ggag      2663
188 <210> SEQ ID NO: 3
189 <211> LENGTH: 328
190 <212> TYPE: PRT
191 <213> ORGANISM: Corynebacterium glutamicum
193 <400> SEQUENCE: 3
195 Met Asn Ser Pro Gln Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly
196 1              5              10              15
199 Ala Ala Gly Gln Ile Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly
200              20              25              30
203 Glu Val Phe Gly Thr Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile
204              35              40              45
207 Pro Gln Ala Leu Gly Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp
208              50              55              60
211 Ser Ala Phe Pro Leu Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn
212 65              70              75              80
215 Glu Ala Phe Asp Gly Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro
216              85              90              95
219 Arg Gly Lys Gly Glu Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys
220              100             105             110
223 Ile Phe Gly Pro Gln Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp
224              115             120             125
227 Ile Arg Val Leu Val Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile
228              130             135             140
231 Ala Ser Ala Ala Ala Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met

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232 145          150          155          160
235 Met Arg Leu Asp His Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu
236          165          170          175
239 Gly Arg Gly Ser Ala Glu Phe Asn Asn Ile Val Val Trp Gly Asn His
240          180          185          190
243 Ser Ala Thr Gln Phe Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu
244          195          200          205
247 Lys Val Thr Asp Leu Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile
248          210          215          220
251 Pro Arg Val Ala Asn Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys
252 225          230          235          240
255 Ser Ser Ala Ala Ser Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp
256          245          250          255
259 Trp Val Gln Gly Thr Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr
260          260          265          270
263 Gly Ala Tyr Gly Ile Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val
264          275          280          285
267 Ser Arg Asn Gly Glu Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp
268          290          295          300
271 Phe Gln Arg Ala Arg Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu
272 305          310          315          320
275 Arg Glu Ala Val Arg Asp Leu Leu
276          325

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279 &lt;210&gt; SEQ ID NO: 4

280 &lt;211&gt; LENGTH: 18

281 &lt;212&gt; TYPE: DNA

282 &lt;213&gt; ORGANISM: Artificial Sequence

284 &lt;220&gt; FEATURE:

285 &lt;223&gt; OTHER INFORMATION: synthetic DNA

287 &lt;400&gt; SEQUENCE: 4

288 aargtyacyg tyacyggy

18

291 &lt;210&gt; SEQ ID NO: 5

292 &lt;211&gt; LENGTH: 17

293 &lt;212&gt; TYPE: DNA

294 &lt;213&gt; ORGANISM: Artificial Sequence

296 &lt;220&gt; FEATURE:

297 &lt;223&gt; OTHER INFORMATION: synthetic DNA

299 &lt;400&gt; SEQUENCE: 5

300 cgrttrtgrt cvarrcg

17

VERIFICATION SUMMARY

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DATE: 07/26/2001

TIME: 15:19:36

Input Set : A:\203979US.txt

Output Set: N:\CRF3\07262001\I903770.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date